

- 1 -

...] NC_000913.ygjN

p35 6.1 bits

... p35-(24)
p35-p10

----- ... p35-p10 3232547 total 4.9

Sequence alignment diagram showing mRNA sequence 3232560 with amino acid translations and predicted secondary structure. The top row shows the mRNA sequence with start sites marked by asterisks (*). The bottom row shows the deduced amino acid sequence. Red dots indicate stop codons. A dashed box highlights a segment starting at position 107, which includes a p10 gene (1.3 bits) and a fMet initiation site.

... p35-(24)-p10 3232547 Gap 2.4 bits
... p35-p10 3232547 total 4.9 bits

The diagram illustrates the tRNA structure, which is L-shaped. The long stem has a green loop at the bottom left labeled "anticodon loop". At the top right, there is a red box labeled "amino acid attachment site". A blue arrow points from the text "Met -" to the attachment site.

```
[redacted] sd-(13)-ir 3232603 Gap 4.6 bits  
[redacted] sd-ir 3232603 ygjN_REPO233+ total
```

|-----| sd-11 3232003 79JN_REF2334 total 6.2 Bits

*3232610 * *3232620 * *3232630 * *3232640 * *3232650 * *3232660 * *3232670 *
 5' c a g g g a t t t t t g t t t a t g g a a g c g c g a t t c c a g a a c t g g g a c a t t g c c g g a t g c g a c g t t g c c g 3'
 - - - - fMet - phe - tyr - gly - ser - ala - ile - pro - glu - leu - gly - arg - his - cys - arg - met - arg - arg - leu - pro -
 alv - ile - phe - cys - phe - met - glu - ala - arg - phe - gln - asn - trp - ala - asp - ile - ala - gly - cys - asp - ala - cys -
 ...
 ir ygjN REP233+